

Query Match	54.18;	Score 1496;	DB 2;	Length 352;
Best Local Similarity	54.38;	Pred. No. 1.11e-195;		
Matches 182;	Conservative	88;	Mismatches 56;	Indels 9;
				Gaps 9;

RESULT	8
ENTRY	S55594
TITLE	G protein-coupled receptor E1 - equine herpesvirus 2
ORGANISM	#formal_name equine herpesvirus 2
DATE	10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Sep-1997

ACCESSION: S55594
 REFERENCE S55594
 #authors Telford, E.A.R.; Watson, M.S.; Alrd, H.C.; Perry, J.
 #journal J. Mol. Biol. (1995) 249:520-528
 #title The DNA sequence of equine herpesvirus 2.
 #accession S55594
 ##status preliminary, nucleic acid sequence not shown
 ##molecule_type DNA
 ##residues 1-383 ##label TEL
 ##cross-references GBR:U20824; NID:g655172; PID:g655173
 G protein-coupled receptor
 #length 383 #molecular-weight 43667 #checksum 1663
 KEYWORDS
 SUMMARY

SEQUENCE COMPARISON

#authors Chato, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
#title Molecular cloning and functional expression of two monocyte
chemoattractant protein 1 receptors alternate
splicing of the carboxyl-terminal tails.
#cross-references MUID:94195821

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FEATURE
#status Preliminary
#molecule_type mRNA
#residues 1-360 #label RES
#cross-references EMBL:U03905; NID:g472557; PID:g472558
GENETICS
#gene GDB:CMKBR2
#cross-references GDB:33764; OMIM:601267
#map_position 3p21-3p21
KEYWORDS
alternative splicing; G protein-coupled receptor;
glycoprotein; transmembrane protein

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43-70	#domain	transmembrane	#status predicted	#label TM1\
81-100	#domain	transmembrane	#status predicted	#label TM2\
115-136	#domain	transmembrane	#status predicted	#label TM3\
154-178	#domain	transmembrane	#status predicted	#label TM4\
207-226	#domain	transmembrane	#status predicted	#label TM5\
244-268	#domain	transmembrane	#status predicted	#label TM6\

	287-309	#domain transmembrane #status predicted #label TM\
	14	#binding_site carbohydrate (asn) (covalent) #status predicted\
	113-190	#disulfide_bonds #status predicted
SUMMARY	Length 360	#molecular_weight 41063 #checksum 1732
Query Match	52.0%	Score 1438; DB 2; Length 360;
Best Local Similarity	53.4%;	Pred. No. 5.17e-187;
Matches 183;	Conservative	87; Mismatches 63; Indels 10; Gaps 8;
Dd	21	TTFEDYDGA PC HKFDVKQIGAOILPPLSLVFI EFGVG NMLVLILNCKRKLCTDIY 80
Oy	14	TSYID-DVGLLCEADTRALMAQFVPPLSVLTFFCLGNVVMMILKYRLRIIMNTIX 72
Dd	81	LNLAI IDLLFLITLP LMASHA-AANEVSGNAMCKFTGLYHGYGCGIFILLTIRY 139
Oy	73	LNLAI IDLLFLITLP MIVHYRGNNVFHGSKLLSGEHLISGFIIILLTIDRY 132
Dd	140	LAIHA VFAFCARIVTEGV STVTMLVAFAFVPGIIFFKCKEDSYVCYPP--R- 196
Oy	133	LAIHA VFAFCARIVTEGV ITSYTWGLALAPLEIFETFEELFEELLSALYPEDIV 192
Dd	197	-GANNFTIMNLI GLVPL LINVIYCSGLIKTLRLCRNEKRRAVRVIFTIMIYELF 255
Oy	193	YSWRHFHTLRMTIFCLVPLPLVMACYTGIIKTLRP--KKRYKAIRLIFVMAVEFIE 251
Dd	256	WTPIVNI VLLTM POEF-FGLSNCSTSDODAAOVPEFLMTCICINPIIYAVERKFR 314
Oy	252	WTPYVVALLESYSOILFG-NDCERTKHLDLYMLVTVIAVSHCAMPYIAFAVGERFK 310
Dd	315	YLSEFRKHITRKFCQCPVRETVDGVTNPSTPGDEVS 357
Oy	311	YLRFHFHRHLMHLGRYIPFLPSKLE-RTSSVSPSTAEBELS 352
RESULT 10	149340	#type complete
ENTRY	MIP-1	alpha receptor like-1 - mouse
TITLE	#formal_name Mus musculus	#common_name house mouse
ORGANISM	02-Jul-1996	#sequence_revision 02-Jul-1996 #text_change
DATE	28-Feb-1997	
ACCESIONS	149340	
REFERENCE	149339	
#authors	Gao, J.L.; Murphy, P.M.	
#journal	J Biol. Chem. (1995)	2:17494-17501
#title	Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.	
#cross-references	MUID:95340546	
#accession	149340	
#status	Preliminary; translated from GB/EMBL/DBJ	
##molecule_type DNA		
##residues	1-356	#label RES
##cross-references EMBL:U028405; NID:g881549; PID:g881550		
#length 356	#molecular_weight 40934	#checksum 563
SUMMARY		
Query Match	51.8%;	Score 1433; DB 2; Length 356;
Best Local Similarity	52.0%;	Pred. No. 2.88e-186;
Matches 173;	Conservative	78; Mismatches 80; Indels 2; Gaps 22
Dd	22	GFLLCFSIN VAFGI TPPLYSLVFTIGYGHVLYVLIOHKRLRMNTSTYLENLASD 81
Oy	21	GLCEKAD TRALMAQ FVPLPSLVFTFGNGVVMMILIKYRLRIIMNTIYNLNLASD 80
Dd	82	LVELSTI PRPVNDYIMKDM TFEGNAOKFVSGFYGLGSDMFITLLTIDRLAVAHVF 141
Oy	81	LLFLVTLPFWIHVYRGNNVFHGSKCLLSGFTHGLSELFIILLIIDRLAIYHAVF 140
Dd	142	ALARATY FGIISII TWLAALVSI PC LVF-KSQMEFTYHCTRALLPKRSILNFLRLO 200
Oy	141	ALRRATY FGVITIS IWMGLAVIALAP-EFIFETDELFEETLCALYPEDIVYSMRHF 199

Db	201	ALTMNLTGILPLPLAMITCYRTTIWLRHRRPKAKWRLFIETVTLLEFLLAPYDAA	260
Qy	154	TLMTTFCLVLPVLAICYTGTITKLRCPSKKYKAIIRLFIYMAVFFIETWPIYNAI	259
Db	261	FVSAFEDVLEFTPSCLSSQOVDLSLMTTEALATYHCCVNPVIVYVGRKFRKYLWOLFRRH	320
Qy	260	LTSYOSILFQNCNCEKTKHLDLMVLTVETVIAASHCCMNPIYIAFGEFRKRYLRHFFRRH	319
Db	321	TAITLPQWLPFLSEDRASARAPLSTVEITMS	353
Qy	320	LLMLHGRYIPFLSEKLETTERTSSVSTAPLELS	352
RESULT	11		
ENTRY	138450	#type complete	
TITLE	Chemokine (C-C) receptor 2, splice form A - human		
ALTERNATE_NAMES	C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractin 1 receptor		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 29-Aug-1997		
ACCESSIONS	138450		
REFERENCE	A53477		
authors	Charo, I.F.; Myers, S.U.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. U.S.A. (1994) 91:2752-2756		
#journal	Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756		
#title	Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.		
#cross-references	MUID:94195821		
#accession	I38450		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-374 #label RES		
#cross-references	EMBL:003882; NID:g472555; PID:g472556		
GENETICS			
#gene	CDB:CMKBR2		
#cross-references	GDB:337364; OMIM:601267		
#map_position	3p21-3p21		
KEYWORDS	alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein		
FEATURE			
44-68	#domain transmembrane #status predicted #label TM1\		
79-99	#domain transmembrane #status predicted #label TM2\		
115-136	#domain transmembrane #status predicted #label TM3\		
154-178	#domain transmembrane #status predicted #label TM4\		
208-226	#domain transmembrane #status predicted #label TM5\		
244-265	#domain transmembrane #status predicted #label TM6\		
292-309	#domain transmembrane #status predicted #label TM7\		
14	#binding_site carbonylstate (7sn) (covalent) #status predicted\		
32-277,113-190	#disulfide_bonds #status predicted		
SUMMARY	#length 374 #molecular_weight 41914 #checksum 5414		
Query Match	48.9%; Score 1352; DB 2; Length 374;		
Best Local Similarity	56.2%; Pred. No. 3,51e-174;		
Matches 168; Conservative	72; Mismatches 50; Indels 9; Gaps 7		
Db	21	TFEFDVDCAPCKPFVKQIGALPPYLSLVFIFGFGNMVYLILNCKRLKCTDIY	80
Qy	14	TSYID-DVGLCEKADTRLMQFPPLXSLVFTGGLGNVYVWMLTKRYLRIMTNY	72
Db	81	LNMLAISDLLEFLLTPLEMAHSA-ANEWFGNACKLFTGLYHIGFGGIFILLTIDRY	139
Qy	73	LNMLAISDLLEFLLTPLEFMHLYVGNHWPVGHCKMCKLLSGFTGTGLYSEIFFILLTIDRY	132
Db	140	LAIVHAVFALKATVTFGVVTSYITPLVAVFASVGCIIFTKQKDSVYVCGPRP--R-	196
Qy	133	LAIVHAVFALKATVTFGVVTSYITPLVAVFASVGCIIFTKQKDSVYVCGPRP--R-	192
Db	197	-GNMNFITIMRNLTIGVLPPLVAVICYSGLITLLCRNKKRHHAVAVETIMVYFLF	255
Qy	193	YSMRHFTLMTTFCLVLPVLAICYTGTITKLRCPS-KKKYKAIIRLFIYMAVFFIETWPIYNAI	251